What is claimed is:

1. An oligonucleotide which selectively hybridizes with a target DNA sequence associated with pathogenic species of *Guignardia*, said oligonucleotide having a sequence selected from the group consisting of AAAAAGCCGCCCGACCTACCT (SEQ ID NO: 1) and TAAAAAAGCCGCCCGACCTAC (SEQ ID NO: 8).

2. An oligonucleotide which selectively hybridizes with non-pathogenic species of *Guignardia*, said oligonucleotide being selected from the group consisting of GCTACAACGCCGAAATGACCTT (SEQ ID NO: 2), GCCGTCGCCCAGCACTC (SEQ ID NO: 3), and GCTACAACGCCGAAATGACC (SEQ ID NO: 9).

3. An oligonucleotide for priming a DNA amplification of a target DNA sequence associated with pathogenic species of *Guignardia*, said oligonucleotide having a sequence selected from the group consisting of AAAAAGCCGCCCGACCTACCT (SEQ ID NO: 1) and TAAAAAAGCCGCCCGACCTAC (SEQ ID NO: 8).

4. An oligonucleotide for priming a DNA amplification of a target DNA sequence associated with non-pathogenic species of *Guignardia*, said oligonucleotide being selected from the group consisting of GCTACAACGCCGAAATGACCTT (SEQ ID NO: 2), GCCGTCGCCCAGCACTC (SEQ ID NO: 3), and GCTACAACGCCGAAATGACC (SEQ ID NO: 9).

5. A method for priming DNA amplification of a target DNA sequence associated with pathogenic species of *Guignardia*, said method comprising:

a) obtaining a DNA sample from a fruit suspected of being infected with *Guignardia*;

b) providing a forward primer selected from the group consisting of SEQ ID NO: 1 and 8;

c) providing a reverse primer selected from the group consisting of SEQ ID NO: 6 and 11; and

d) subjecting said DNA sample and said forward and reverse primers to conditions suitable for polymerase chain reaction, amplification of said DNA in the presence of said primers indicating infection with a pathogenic *Guignardia* species.

6. A method for differentiating pathogenic species of *Guignardia* from non-pathogenic species of Guignardia, comprising the steps of:

a) obtaining a DNA sample from a *Citrus* fruit suspected of being infected with *Guignardia*;

b) contacting said DNA with a detectably labeled probe which selectively hybridizes with said DNA, said probe having the sequence of SEQ ID NO: said probe having a sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 8, AND SEQ ID NO:9; and detecting specific hybridization if any, samples demonstrating hybridization with SEQ ID NO: 1 or SEQ ID NO: 8 being indicative infection of the *Citrus* fruit with pathogenic *Guignardia* and samples demonstrating hybridization with SEQ ID NOS: 2, 3, or 9 being indicative of infection of the *Citrus* fruit with non-pathogenic species of *Guignardia*.

7. A method for differentiating pathogenic species of *Guignardia* from non-pathogenic species of *Guignardia*, comprising the steps of:

a) obtaining a DNA sample from a *Citrus* fruit suspected of being infected with *Guignardia*;

b) immobilizing said DNA sample on a solid support;

c) probing said immobilized sample DNA with a detectably labeled probe, said probe having a sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 8, AND SEQ ID NO:9; and

d) assessing said solid support for hybridization of said probe to said immobilized DNA, samples demonstrating hybridization with SEQ ID NO: 1 or SEQ ID NO: 8 being indicative infection of the *Citrus* fruit with pathogenic *Guignardia* and samples demonstrating hybridization with SEQ ID NOS: 2, 3, or 9 being indicative of infection of the *Citrus* fruit with non-pathogenic species of *Guignardia*.

8. A method of screening for *Citrus* Black Spot disease, said method comprising

a) obtaining a nucleic acid sample; and

b) assaying the nucleic acid sample for the presence of a sequence which hybridizes with SEQ ID NO: 1 or SEQ ID NO: 8 or SEQ ID NO: 4, wherein the presence of said hybridizing sequence is indicative of pathogenic *Guignardia* infection causing *Citrus* Black Spot disease.

9. A method in accordance with claim 5, wherein said assaying further comprises amplification

of the ITS region of *Guignardia* rDNA containing an ITS nucleic acid, said ITS nucleic acid sequence being amplifiable using primers consisting of SEQ ID NO: 12 and SEQ ID NO: 13.

10. A method in accordance with claim 5, wherein said polymerase chain reaction is primed by SEQ ID NOS: 8 and 11.

11. A kit for use in screening for *Citrus* Black Spot disease comprising a pathogen-specific oligonucleotide probe immobilized on solid matrix, and further comprising means for amplifying a test samples's nucleic acid encoding all or part of the rDNA gene, wherein said test sample's nucleic acid comprises a sequence of SEQ ID NO: 4.

12. A kit in accordance with claim 11, wherein said amplifying means comprises:
(a) a primer pair of oligonucleotides comprising a first oligonucleotide having the sequence of SEQ ID NO: 1 or SEQ ID NO: 8 and a second oligonucleotide having the sequence of SEQ ID NO: 6 or SEQ ID NO: 11; and
(b) reagents necessary to perform PCR.

13. A kit in accordance with claim 12, wherein the oligonucleotide pair comprises SEQ ID NO: 8 and SEQ ID NO: 11.

14. A kit for use in screening for non-pathogenic *Guignardia* species comprising a non-pathogen-specific oligonucleotide probe immobilized on solid matrix, and further comprising means for amplifying a test samples's nucleic acid encoding all or part of the rDNA gene, wherein said nucleic acid comprises a sequence of SEQ ID NO: 5.

15. A kit in accordance with claim 14, wherein said amplifying means comprises:
(a) a primer pair of oligonucleotides comprising a first oligonucleotide having the sequence of SEQ ID NO: 2 or SEQ ID NO: 9 and a second oligonucleotide having the sequence of SEQ ID NO: 6 or SEQ ID NO:10 or SEQ ID NO: 11; and
(b) reagents necessary to perform PCR.

16. A kit in accordance with claim 15 wherein the oligonucleotide pair comprises SEQ ID NO: 9 and SEQ ID NO: 10.

17. A method for identifying pathogenic *Guignardia* species in a sample, said method comprising the steps of:
a) culturing *G. citricarpa;*
b) subjecting said cultured *G. citricarpa* to conditions which effect lysing of said *G. citricarpa,* thereby releasing DNA from said hyphae;
c) contacting said released DNA with a primer pair of oligonucleotides comprising a first oligonucleotide having the sequence of SEQ ID

NO: 1 or SEQ ID NO: 8 and a second oligonucleotide having the sequence of SEQ ID NO: 6 or SEQ ID NO: 11 under conditions where amplification of pathogenicity-associated ITS sequences occurs, if said pathogenic *Guignardia* is present in said sample; and

d) detecting said amplified sequence, if present.

18. A method as claimed in claim 17, wherein said amplified sequence is detected via incorporation of a detectable label.

19. A method as claimed in claim 17, wherein said amplified sequence is detected by gel electrophoresis of said amplified sample.

20. A method as claimed in claim 17, wherein said ITS sequences are amplified using a primer set having SEQ ID NOS: 12 and 13 prior to amplification of pathogenicity related sequences employing a primer set having SEQ ID NO: 8 and 11.

21. A method for identification of pathogenic *Guignardia citricarpa*, said method comprising:

a) contacting a tissue section containing a black spot lesion with a permeabilization agent;

b) contacting said permeabilized lesion DNA with a detectably labeled oligonucleotide having a sequence of SEQ ID NO: 1 or SEQ ID NO: 8; and

c) detecting hybridization of said oligonucleotide to said DNA, if any, said hybridization indicating the presence of pathogenic *G. citricarpa*.